



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

1637 \$
#25/105

Application of: Selifonov, et al

Attorney Docket No.: MXGNP002X1

Application No.: 09/495,668

Examiner: Young J. Kim

Filed: February 1, 2000

Group: 1637

Title: METHODS OF POPULATING DATA
STRUCTURES FOR USE IN EVOLUTIONARY
SIMULATIONS

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CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service as First Class Mail to: Commissioner for Patents, Washington, DC 20231 on September 13, 2002.

Signed: _____

Leslie Russell

**INFORMATION DISCLOSURE STATEMENT
AFTER FINAL ACTION OR NOTICE OF ALLOWANCE
(37 CFR §§ 1.56 AND 1.97(d))**

Commissioner for Patents
Washington, DC 20231

Dear Sir:

The references listed in the attached PTO Form 1449, a copy of which is attached, may be material to examination of the above-identified patent application. Applicants submit this reference in compliance with their duty of disclosure pursuant to 37 CFR §§ 1.56 and 1.97. The Examiner is requested to make this citation of official record in this application.

This Information Disclosure Statement is not to be construed as a representation that a search has been made, that additional information material to the examination of this application does not exist, or that this reference indeed constitutes prior art.

This Information Disclosure Statement is being filed after the mailing date of final action under §1.113 or a notice of allowance under §1.311, but before payment of the issue fee.

Accompanying this Information Disclosure Statement is the fee set forth in 37 CFR

1.17(p).

The undersigned hereby states:

If fees are due, enclosed is our Check No. 6231 for \$180.00 in payment of the Information Disclosure Statement Fee. If it is determined that any additional fees are due, the Commissioner is hereby authorized to charge such fees to Deposit Account 500388 (Order No. MXGNP002X1).

Respectfully submitted,

BEYER WEAVER & THOMAS, LLP

A handwritten signature in black ink, appearing to read "Jeffrey K. Weaver", with a long horizontal flourish extending to the right.

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Form 1449 (Modified) Information Disclosure Statement By Applicant (Use Several Sheets if Necessary)	Atty Docket No: MXGNP002X1	Application No.: 09/495,668
	Applicant: Selifonov et al. Filing Date February 1, 2000	Group 1631

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U.S. Patent Documents

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Examiner Initial	No.	Patent No.	Date	Patentee	Class	Sub-class	Filing Date
	A1	6,125,331	9/26/00	Toh			
	A2	6,403,312	6/11/02	Bassil, et al			
	A3						

Foreign Patent or Published Foreign Patent Application

Examiner Initial	No.	Document No.	Publication Date	Country or Patent Office	Class	Sub-class	Translation	
							Yes	No
	B1	WO00/47612	8/17/00	WIPO				
	B2	WO01/61344	8/23/01	WIPO				
	B3	WO00/42559	7/2/00	WIPO				
	B4	WO01/75767	10/11/01	WIPO				

Other Documents

Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	C1	Young et al., "Characterization of Receptor Binding Determinants of Granulocyte Colony Stimulating Factor," <i>Protein Science</i> 6:1228-1236, 1997
	C2	Dahiyat and Mayo, "Protein Design Automation," <i>Protein Science</i> , 5:895-903, (1996)
	C3	Su et al., "Coupling Backbone Flexibility and Amino Acid Sequence Selection in Protein Design," <i>Protein Science</i> , 6:1701-1707, (1997)
	C4	Voigt et al., "Computationally Focusing the Directed Evolution of Proteins," <i>Journal of Cellular Biochemistry Supplement</i> , 37:58-63 (2001)
	C5	Hellberg et al., "Minimum Analogue Peptide Sets (MAPS) for quantitative Structure-Activity Relationships," <i>Int. J. Peptide Protein Res.</i> 37:414-427 (1991)

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	C6	Martin van Heel, "A New Family of Powerful Multivariates Statistical Sequence Analysis Techniques," J. Mol. Biol, 220:877-887 (1991)
	C7	Goldman et al., "Estimating Protein Function From Combinatorial Sequence Data Using Decision Algorithms and Neural Networks," Drug Dev. Research 33:125-132 (1994)
	C8	Gustafsson et al., "Exploration of Sequence Space for Protein Engineering," J. Mol. Recognit. 14:308-314 (2001)
	C9	Miyazawa et al., "Residue-Residue Potentials with a Favorable Contact Pair Term and an Unfavorable High Packing Density Term, for Simulation and Threading," J. Mol. Biol., 256:623-644 (1996)
	C10	Chao Zhang, "Extracting Contact Energies From Protein Structures: A Study Using a Simplified Model," Proteins: Structure, Function, and Genetics, 31:299-308 (1998)
	C11	Miyazawa et al., "Self-Consistent Estimation of Inter-Residue Protein Contact Energies Based on an Equilibrium Mixture Approximation of Residues," Proteins: Structure, Function, and Genetics, 34:49-68 (1999)
	C12	Miyazawa et al., "An Empirical Energy Potential With a References State for Protein Fold and Sequence Recognition," Proteins: Structure, Function, and Genetics, 36:357-369 (1999)
	C13	Moore et al., "Predicting Crossover Generation in DNS Shuffling," PNAS, Vol. 98, No. 6, 3226-3231 (2001)
	C14	Lehman et al., "Engineering Proteins for Thermostability: the Use of Sequence Alignments Versus Rational Design and Directed Evolution," Current Opinion in Biotechnology, 13:371-375 (2001)
	C15	Colleen Kelly, "A Test of the Markovian Model of DNA Evolution," Biometrics 50, 653-664, (1994)
	C16	H.W. Hellenga, "Rational Protein Design: Combining Theory and Experiment," Proc. Natl. Acad. Sci. USA, Vol. 94, pp. 10015-10017, (1997)
	C17	William F. DeGrado, "Proteins from Scratch," Science, Vol. 278, 80-81 (1997)



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	C18	Jonsson, et al, "Quaintitative Sequence-Activity Modeils (QSAM)- Tool For Sequence Design", Nuclear Acid Research Vol. 21, No. 3, pp. 733-739 (1993)
	C19	Sjostrom, et al, "Signal Peptide Amino Acid Sequences In <i>Escheruchua coli</i> Contain Information Related To Final Protein Localization. A Multivariate Data Analysis", The CMBO Journal vol. 6, no. 3, pp 823-831, (1987)
	C20	Patel, et al, "Patenting Computer-Designed Peptides", Journal Of Computer-Acid Molecular Design 12 pp543-556, (1998)
	C21	Schneider, et al, "Peptide Design by Artificial Neural Networks and Computer-Based Evolutionary Search", Proc. Natl. Acad. Sci. USA, vol. 95, pp. 12179-121184, October 1998
	C22	Mee, et al, "Design of Active Analogues of a 15-Residue Peptide Using D-Optimal Design QSAR and a Combinatorial Search Algorithm", J Peptide Res. 49, pp. 89-102, (1997)
	C23	Bogarad, et al, "A Hierarchical Approach to Protein Molecular Evolution", Proc. Natl. Acad. Sci. USA, Vol. 96, pp. 2597-2595, March 1999
	C24	Darius, et al, "Simulated Molecular Evolution" Or Computer-Generated Artifacts?", Biophysical Journal, Vol. 67, pp. 2120-2122, November 1994
Examiner		Date Considered

Examiner: Initial citation considered. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.